

Db 1741 CAAAAAAAAAAAAA 1753

RESULT 4
AK024798
LOCUS AK024798 1577 bp mRNA linear PRI 29-SEP-2000
DEFINITION Homo sapiens cDNA: FLJ21145 fis, clone CAS08741.
ACCESSION AK024798
VERSION AK024798.1 GI:10437188
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens primary smooth muscle cells of human coronary artery
cDNA to mRNA, clone_lib:CAS clone:CAS08741.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Watanabe,K., Kumagai,A., Itakura,S., Yamazaki,M., Tashiro,H.,
Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,
Nakamura,Y., Isogai,T. and Sugano,S.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished (2000)
REFERENCE 2 (bases 1 to 1577)
AUTHORS Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
Shibahara,T., Tanaka,T. and Nakamura,Y.
TITLE Direct Submission
JOURNAL Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure Analysis, Human
Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing; Research Association for Biotechnology; cDNA library
construction, 5' & 3'-end one pass sequencing; Department of
Virology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
Agency).
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CAS08741"
/cell_type="primary smooth muscle cells of human coronary
artery"
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/note="cloning vector pME18SFL3"
CDS 69. 1169
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/db_xref="GI:10437189"
/translation="MAVLALTDLSADMKARLGRMVVASDKSGQPVTADDLGVGTGALT
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LVADGCCNLQKQIQITQLFGVPVVVALNVFKTDTRAIEDLVCELAKRAGAFDAVPCYH
WSVGGKGSVDLARAVREAAASKRSRFLYDVQVPIVDKIMTIAQAVYGAKDIELSPEA
QAKIDRYTQGGFCNLPICMAKTHLSLHQDPDKGVPRDFILPISDVRSIGAGFIYPL
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BASE COUNT 424 a 336 c 420 g 397 t
ORIGIN

Query Match 42.8%; Score 1565.6; DB 9; Length 1577;
Best Local Similarity 99.7%; Pred. No. 1.9e-274;
Matches 1568; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 1 GGCAGGGAAACACAGAGAAGGCCATTACCGGACGGCGCAGTTTGACATCGCAGTGCCCA 60
Qy 2146 gcgagatcatggcgggtgctggccctgacggacagcctcgagacatgaaggcacggctgg 2205
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| Db | 121 | GAAGAGATGTGTGTGTGCCAGTACCAAAACGGGACACCTGTACAGCAATGATTTGGGGG | 180 |
| QY | 2266 | tgaacagtgctttacagatttttgatgaaagatgtcaataaaaccaaactgtatgcagccc | 2325 |
| Db | 181 | TGACAGGTGCTTTGACATGTTTGATGAAAGATGTCAATTAACCAACCTGTATGCGACACC | 240 |
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| Db | 241 | TGGAAAGGACACACTGTGTGTGTGGCATGTGGGGCCCTTTTGTACATTGTCTACGGCAACT | 300 |
| QY | 2386 | cttcagtgcttggtctgataaaattgcccctgaaactgtgttctgaaagaagatttgaatga | 2445 |
| Db | 301 | CTTCAGTGTGGCTGATTAATAATTGCCCTGAAACTGGTTGCTGAAAGAGATTTGTAGTGA | 360 |
| QY | 2446 | ccgaaagctgacctttgtgtctgacacatcggaatggagaaaattctcaacatcaagtccggg | 2505 |
| Db | 361 | CCGAAGCTGGCTTTTGTGTGCTGACATCGGAAATGAGAAATTTCTTCAACATCAAGTCCGAG | 420 |
| QY | 2506 | cttcggagcttggtgtcccaacgtgtgttgtttagtggccaaggtgtcgagctctgaagaatgc | 2565 |
| Db | 421 | CTTCCGGCTGTGGTGCACCAACGTGTGTGTGTAGTGGCAACGGTGCACGCTGTGAAGATGC | 480 |
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| Db | 481 | ATGGAGCGCGGGCCAAAGTGTAAAGCGCTGTGTCTCTTAAAGAAAGATATTACAGAGGAGA | 540 |
| QY | 2626 | acatccaagctgtgtgccaagaagcgtgctgttaacccccaagaagcaaatccaatcaactcagc | 2685 |
| Db | 541 | ACATCCAGCTGTGTGCAGACAGCGCTGTGTACCTCCACGAAGCAAAATTCAAGATCACTACAC | 600 |
| QY | 2686 | tctttaggggttccgtttgtgtgtgctctgaatgtctcaagcagccacccgctgtgaga | 2745 |
| Db | 601 | TCTTTGGGCTTCCCGTTGTGTGTGTGCTCTGAATGTCTTCAAGACGACACCCGGCGTGAGA | 660 |
| QY | 2746 | ttgacttggtgtgtgagacttgcaaagcgggtgtgtgctcttgatgtcaatccctgtctatc | 2805 |
| Db | 661 | TTGACTTGTGTGTGTGACTTGTGCAAACCGGGCGGTGTCCCTTGTATGAGAGTCCCTGTGATTC | 720 |
| QY | 2806 | actgtgctcggttgtgtgaaagaagatcgtgtgaactgtgctcggtgctgtgagaagagctgcga | 2865 |
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| QY | 2866 | gttaaaagaagccgattccagttccgttatagtatgttcaagttccaattgtgtgacaagataa | 2925 |
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| Db | 841 | TGACCAATTGCTCAGGGCTGTATGAGAGCCAAAGATATTGAACCTCTCTGTAGGACACAG | 900 |
| QY | 2986 | ccaaaatagatcgtttacactccaacagggttttggaaattggccatatgtatgtgacaaga | 3045 |
| Db | 901 | CCAAAAATAGATCTTACACTCAACAAGGTTTGGAAATTTGGCCCATGTGCATGGCAANA | 960 |
| QY | 3046 | ccaacactttctacatctcaaccaacttgcacaaaagaatgtgtgccaagagacttaacttacc | 3105 |
| Db | 961 | CCCAACCTTCTCTATCTCACCAACCTGCACAAAAAAGGTGTGCCAAGGAGACTTCATCTTAC | 1020 |
| QY | 3106 | ctatcagtgacgtcccggtccaagatagagcgtgtgtcatttacccttggttggaagca | 3165 |
| Db | 1021 | CTATCACTGATGACGTCCGGGCGACGATTAAGCCGTGGGTTCATTATACCTTTGGTCCGAAGA | 1080 |
| QY | 3166 | tgaagcaactgtgccagagctgccaccccgccctgtcttattgacatagatattgatacgg | 3225 |
| Db | 1081 | TGAGCACTCAATGCCAGACTGCCACCCGGCCCTCTTTTATGACATAGATCTTGATACCG | 1140 |
| QY | 3226 | aaacagaacaagtataaagcttgttctaagtgtgacaagagctctcaacagagaccgatgag | 3285 |
| Db | 1141 | AAACAGAACAAAGTTAAAGGCTTGTCTTAAAGTGAGCAAGGCTCTCACAGACCCGATGTGAG | 1200 |

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| QY | 3286 | actccctgaagaagcactactcttcgccccttttgcctgcagcttggagaaagaaactgaattga | 3345 |
| Db | 1201 | ACTCCTGAACAGACACTACTCTTTGCCCTTTTTCGCGACGCTGGAGAAAGAAACTGAATTGGA | 1260 |
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| Db | 1261 | AAAATGCTGTGTATNGCAATGCTGGAGACATNGTGAATATAGGCCAAAGATTCTCTTCGT | 1320 |
| QY | 3406 | tcaagatgaattctgcttcacagtgagagatgltglttggcctaaagagacctccaccaagac | 3465 |
| Db | 1321 | TCAAGATGAATTCCTGTCACAGTGAAGATNGTGTTCGGCAAAAAGACCTCCACACAGAC | 1380 |
| QY | 3466 | tgaagaaacaaacttaattcttgccttcctggagttccatattcttaactgcctaacact | 3525 |
| Db | 1381 | TGAAGAAACAACTAATTTATTTCTGTTCTGTGGAGTTTCCATTATTTCTACTGCTTACACT | 1440 |
| QY | 3526 | ttagaatgttatatttaatggagactaaaggaattagagatgltgnaactaaaggtaacatt | 3585 |
| Db | 1441 | TTAGAAATTGTTATTTTATTAAGGGGACTAAGGGAATTAAAGCTGTGAAGCTAAAGSTAAACATTT | 1500 |
| QY | 3586 | tcacactcacaagtttcttactattgctcttgaacatgaaataaacatgactctagaanaac | 3645 |
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| Db | 1561 | AAAAAAAAAAAAA 1572 | |

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| | RESULT | 5 |
| LOCUS | AC103974 | |
| DEFINITION | AC103974 Homo sapiens chromosome 11 clone RP11-1081L13 map 11, | HTG 27-JAN-2002 WORKING DRAFT |
| ACCESSION | AC103974 | |
| VERSION | AC103974.3 | GI:18377266 |
| KEYWORDS | QTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP. | |
| SOURCE | human. | |
| ORGANISM | Homo sapiens | |
| Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | |
| REFERENCE | 1 (bases 1 to 186307) | |
| AUTHORS | Birren,B., Linton,L., Nusbaum,C. and Lande,E. | |
| TITLE | Homo sapiens chromosome 11, clone RP11-1081L13 | |
| JOURNAL | Unpublished | |
| REFERENCE | 2 (bases 1 to 186307) | |
| AUTHORS | Birren,B., Linton,L., Nusbaum,C., Lande,E., Ali,A., Allen,N., Anderson,S., Bana,N., Bastien,V., Boguski,J.T., Bonkaghter,B., Brown,A., Camarata,T., Campopiano,A., Chang,Y.J., Chararo.B., Choedel,Y., Colangelo,M., Collins,K., Collamore.A., Cook,R., Cook,P., Deavelano.K., Dewar,K., Diaz,J.S., Dodge,S., Ferro,S., Ferris,P., Fitzlugh,W., Gage,D., Galagan,J., Gaddya,S., Gand,S., Gord,S., Guyette,M., Graham.L., Grand-Pierre.N., Hagos,B., Heardof,A., Horton.L., Hulme.M., Iliev,I., Johnson.R., Jones.C., Kamat,A., Karatas,A., Kells.C., Larocque.K., Iamarezas,R., landers T., Lehoczy,J., Levine,R., Liu.G., Maclean,C., Macdonald.P., Major,J., Marguis N., Matthews.C., McCarthy,M., McKwan,F., McKeenan,K., MCPheeters.R., Meldrum,J., Meneus,L., Mihova,T., Mlenka.V., Murphy,T., Naylor,J., Nguyen.C., Norbu.C., Norman.C.H., O'Connor.T., O'Donnell.P., O'Neill.D., Oliver,J., Peterson.K., Phunhkhap,P., Pierre.N., Pollara.V., Raymond.C., Retta,R., Riback.M., Riley.R., Rise.C., Rogov.P., Roman,J., Roselli.N., Roy A., Santos R., Schauer,S., Schnuppck,R., Seaman,S., Severy,P., Spencer.B., Strange-Thomann,N., Stojanovic.N., Stichaus,N., Sudrmanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigillo,J., Vassiliev,G., Viel,R., Vo,A., Wilson.B., Wu,X., Wyman.D., Ye.W.-J., Young,G., Zainoun,J., Zembek,L., Zimmer.A. and Zody.M. | |
| TITLE | Direct Submission | |
| JOURNAL | Submitted (01-DEC-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA | |
| COMMENT | On Jan 27, 2002 this sequence version replaced gi:18308578. All repeats were identified using RepeatMasker: | |

| | | | | | |
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| 74 | 198.2 | 5.4 | 1803 | 1 | AB006079 |
| 75 | 195.4 | 5.3 | 121 | 10 | MM006665 |
| 76 | 193.8 | 5.3 | 1056 | 1 | AF295724 |
| 77 | 193.6 | 5.3 | 15428 | 1 | AE001815 |
| 78 | 192.8 | 5.3 | 347050 | 1 | AL591981 |
| 79 | 192 | 5.3 | 1056 | 1 | AF295711 |
| 80 | 190.6 | 5.2 | 2034 | 1 | SM039612 |
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| 82 | 181.8 | 5.0 | 1098 | 1 | AF295712 |
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| 85 | 178.6 | 4.9 | 1056 | 1 | AF295713 |
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| 91 | 175.2 | 4.8 | 1050 | 1 | AF295720 |
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| 93 | 175.2 | 4.8 | 1056 | 1 | AF295717 |
| 94 | 175 | 4.8 | 10869 | 1 | AE007816 |
| 95 | 174.4 | 4.8 | 3259 | 1 | AF270090 |
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| 108 | 162.8 | 4.6 | 1098 | 1 | AF459463 |
| 109 | 162 | 4.4 | 1338 | 1 | AF459460 |
| 110 | 161.6 | 4.4 | 1341 | 1 | AF295703 |
| 111 | 161.2 | 4.4 | 1056 | 1 | AF295701 |
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| 113 | 159.4 | 4.4 | 1098 | 1 | AF459458 |
| 114 | 158.8 | 4.3 | 323930 | 1 | AP003194 |
| 115 | 156.4 | 4.3 | 1098 | 1 | AF459459 |
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| 117 | 152.4 | 4.2 | 166426 | 9 | AL136317 |
| 118 | 152.4 | 4.2 | 180057 | 2 | AL445665 |
| 119 | 152.4 | 4.2 | 194487 | 2 | AL591379 |
| 120 | 151 | 4.1 | 1098 | 1 | AF459457 |
| 121 | 149.8 | 4.1 | 170337 | 9 | AL137070 |
| 122 | 147.6 | 4.0 | 68769 | 2 | AC102590 |
| 123 | 138 | 3.8 | 1056 | 1 | AF295714 |
| 124 | 138 | 3.8 | 303040 | 1 | AP000991 |
| 125 | 134.4 | 3.7 | 67272 | 1 | ZMNMRKP |
| 126 | 129.8 | 3.5 | 3713 | 6 | AF269740 |
| 127 | 129.8 | 3.5 | 3713 | 6 | AX145058 |
| 128 | 127 | 3.5 | 288 | 6 | AX307796 |
| 129 | 125 | 3.4 | 66291 | 2 | AC103928 |
| 130 | 125 | 3.4 | 268356 | 2 | FAICID5 |
| 131 | 118.4 | 3.2 | 710 | 1 | AF459456 |
| 132 | 118 | 3.2 | 1056 | 1 | AF295710 |
| 133 | 113.8 | 3.1 | 34178 | 2 | AC101692 |
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| 135 | 104 | 2.8 | 21708 | 2 | AC109541 |
| AB006079 Sphingomo | | | | | |
| 006665 Mus musculu | | | | | |
| AF295724 Unculture | | | | | |
| AE001815 Thermotog | | | | | |
| AL591981 Listeria | | | | | |
| AF295711 Unculture | | | | | |
| U39612 Streptococ | | | | | |
| AF459462 Unculture | | | | | |
| AF295712 Unculture | | | | | |
| AF295704 Thermodna | | | | | |
| AL048694 Human DNA | | | | | |
| AF295713 Unculture | | | | | |
| AF295716 Unculture | | | | | |
| AF295719 Unculture | | | | | |
| AL359638 Homo sapi | | | | | |
| AF295722 Unculture | | | | | |
| AF295706 Eubacteri | | | | | |
| AF295720 Unculture | | | | | |
| AF295721 Unculture | | | | | |
| AF295717 Unculture | | | | | |
| AE007816 Clostridi | | | | | |
| AF270090 Staphyloc | | | | | |
| AX145408 Sequence | | | | | |
| AF295707 Ruminococ | | | | | |
| AF295723 Unculture | | | | | |
| AB026196 Lithosper | | | | | |
| AF295718 Unculture | | | | | |
| AF295702 Clostridi | | | | | |
| AP003314 Staphyloc | | | | | |
| AP003363 Staphyloc | | | | | |
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| AF295705 Homo sapi | | | | | |
| AF295703 Clostridi | | | | | |
| AF459463 Unculture | | | | | |
| AF459460 Unculture | | | | | |
| AF295703 Clostridi | | | | | |
| AF295701 Acetobact | | | | | |
| AF295715 Unculture | | | | | |
| AC084139 Homo sapi | | | | | |
| AF459458 Unculture | | | | | |
| AP003194 Clostridi | | | | | |
| AF459459 Unculture | | | | | |
| AF459461 Unculture | | | | | |
| AL136317 Human DNA | | | | | |
| AL445665 Homo sapi | | | | | |
| AL591379 Homo sapi | | | | | |
| AF459457 Unculture | | | | | |
| AL137070 Human DNA | | | | | |
| AC102590 Mus muscu | | | | | |
| AF295714 Unculture | | | | | |
| AP000991 Thermopila | | | | | |
| X84019 z. mobilis g | | | | | |
| AF269740 Staphyloc | | | | | |
| AX145058 Sequence | | | | | |
| AX307796 Sequence | | | | | |
| AC103928 Mus muscu | | | | | |
| AL445067 Thermopila | | | | | |
| AF459456 Unculture | | | | | |
| AF295710 Proteus v | | | | | |
| AC101692 Mus muscu | | | | | |
| U48882 Streptococ | | | | | |
| AC109541 Rattus no | | | | | |

```

VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
gene
CDS
polyA_signal
polyA_site
BASE COUNT
ORIGIN

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OY 676 agcgtgctgacatcaatcatttgctccctccatagacgtgagcggagat 735
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Db 718 TTGGGTGTGCTCCAGAAATCAATTTGGTGTGACTCATTTGAAGAAAGATGTGATTC 777
OY 1276 tccctgtgagctctcgaattcagaacatgtagtagtagtagtagtagtagtagtag 1335
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Db 898 CAAGTGACATTTGACATTTCAAGAGSACAAATCCAAAAGCTGTGATCTCTTGCAAGG 957
OY 1456 agattgattgtctgcagatgaatgaatctatgtgcaaaagcaaaagcaaaagtaagt 1515
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Db 958 AGATTGATGCTGTGACATGAATAATGAAATCTATGCAAAAGCAAAACCCAAAGTACTT 1017
OY 1516 tgttcgtgtctagaaggttaagaatgaagacagatggaataatgcttaattgttgg 1575
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Db 1018 TGTCTGTGCTAGAAAGGTTAAAGATCAAGCAGATGGAATAATACCTCTTATGTTGCTG 1077
OY 1576 tcaacccacccctcttgagaaggaagacagacagacacacacacacacacacacac 1635
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Db 1138 TCACGCGACACCTGAAATGCAACTCTTGTGCTGTGAGGAGCGCTTCCCAAGAGACGA 1197

OY 1696 cgtttgagtgaaaggaagcgcggtgtgtgatatgccccagtcaccccaatgagag 1755
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Db 1198 CTTTGGAGTGAAGAGAGAGACCGGGGTGTGATATGCCCAGATATCCCATGAGAGG 1257
OY 1756 agttcaacttcaacttgcagtgagacatccacgcacatccacgcgtgcacaaactgtctg 1815
| | | | |
Db 1258 AGTTCAACCTTCACTGTGACTGAGACATCCAGCCATCACCGCTTCCCAATCTTGTG 1317
OY 1816 ctgcgcacatcgacacagagattcttcaagaacacgcaacagataagctctgata 1875
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Db 1318 CTGCGGCATGACACGAGATTTCTTCAATGAATAACCCAAACAGATTAAGCTCTGTATA 1377
OY 1876 atcgcgtgttccctttagtgaatgtgtcagaagaatttccagaatcagcttgcgcg 1935
| | | | |
Db 1378 ATCGGCTGTCTCTTATGAAATGCTGACAGAAATTTCAAGAAATTCAGCTTGCCTCGC 1437
OY 1936 taataaaactggaataaataagatggtccgagacacatcaacagaagaagaatgagta 1995
| | | | |
Db 1438 TAAAAAACTGGAAATTAATTAAGCTGATCCAGCACTGTACAGAAAGAGAGATGA 1497
OY 1996 aatttgccgctcgcacatcccatctacatcagtgagagagatlatgatacaa 2055
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Db 1558 ATGACCGATTTTACAAAAATTAACATCGGCGAGGAAACACAGAAAGGCGCATTTACC 1617
OY 2116 ggcagcgcagtttgacatcgagctgagcagagatcaatgacggtgtcgtgcccctgacg 2175
| | | | |
Db 1618 GCGAGCGCAGATTGTGACATCGCAGTGGCAGAGATCATGCGGCTGTGCGCTGACGG 1677
OY 2176 acagcctcgacagacatgaagacacgcgtggaagagatgtgtgtgcccagtgacaaagc 2235
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Db 1678 ACAGCCTCCAGCATGAAGAGCAGCGCTGGAGAGTGTGTGTGCGCAATGCAAAAGG 1737
OY 2236 ggcagccttgaagagatgtattgtgggtgacaaagtgtcttgacagtttgatgaag 2295
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OY 2356 gcccttctgtaacattgtctcaagcagacatctcaatgttgggtgataaattgccccta 2415
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OY 2416 aactgtgtgtgaagaagattgttagtgacgaagctgtgcttgtgtgacatcgaa 2475
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OY 2476 tgaagaattcttcaacatcaatgaatgcccagcttccggtgtgtgtgccaaagtgtgtgt 2535
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Db 1978 TGGAGAAATTTCTCAATCAATGAAGTCCGACCTTCCGCTTGGGCCCAAGGCTGTGTGT 2037
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Db 2038 TAGTGGACACGCTGAGGCTCTGAAGATGATGAGGCGGGCCAAAGTGAACGCTGTGTG 2097
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OY 2716 atgtcttcaagac 2775
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Db 2218 ATGTCTTCAACACGACACACCGCGCTGAGATTTGACTTGTGTGTGACCTTGTCAAAAGCGG 2277
OY 2776 ctgtgtcctttagtagcagtcctccctgtctatcactgtgtgtgtgtgaagaagatcgtgtg 2835

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Db 2278 CTGGTGCCCTTTGATGCAGTCCCCTGCTATCACTGGTCCGTGGTGGAAAAGGATCGGTGG 233:
Dy 2836 acttggctcgggctgtgagagaggctgcgagttaaagaagccgattccagttccctgtatg 2895
Db 2338 ACTTGGCTCGGGCTGTGAGAGAGGCTGCCAGTAAAGAAGCCGATTCCAGTTCCTGTATG 2397
QY 2896 atgttcagggttccaattgttgacaagataaggaccattgtctcaggctgtcttatggagcca 2955
Db 2398 ATGTTACAGGTTCCAATTGTGGACAAGATAAGGACCATTGTCTCAGGCTGTCTATGGAGCCA 2457
QY 2956 aagatatatgaactctctcctgaggcacaaagccaaaatagatcggttacactcaacagggtt 3015
Db 2458 AAGATATTGAACCTCTCTCTGAGGCACAAGCCAAAAATAGATCGTTACACTCAACAGGGTT 2517
QY 3016 ttggaatttggccatctcatggcacaagaccacctttctctatctcaccaacctgaca 3075
Db 2518 TTGGAAATTGCCCCATCTGCATGGCAAAGACCCACCTTTCTCTATCTCACCAACTGACA 2577
QY 3076 aaaaaagggttgccaagggaacttcatcttaacctatcagtgacgtccgggccagcataggcg 3135
Db 2578 AAAAAGGTGTGCCAAGGGACTTCATCTTACCTATCAGTGACGTCCGGGCCAGCATAGGCG 2637
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QY 3436 ggtgttcggcaaaaaggacctccaccaagactgaaagaaactaatttatttctgtttctgt 3495
Db 2938 GGTGTTTCGGCAAAGGACTCCACCAAGACTGAAAGAACTAATTTATTCTGTTCTGT 2997
QY 3496 ggagtttccattatttctactgtcttacactttaagaatgtttattttatggggactaagg 3555
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Db 3058 ATTAGGAGTGTGAACATAAAGGTAACATTTCCACTCTCAAGTTTCTACTTTGTCTTTG 3117
QY 3616 aactgaaaataaacatggatctagaaaacccccccccccccccc 3657
Db 3118 AACTGAAAATAAACATGGATCTAGAAAACCAAAAAAAAAAAAAA 3159

RESULT 2
BC017477
LOCUS
DEFINITION BC017477
Homo

```

RESULT      2
BC017477
LOCUS
DEFINITION  BC017477
              Homo sapiens, Similar to 2749 bp mRNA linear PRI 21-NOV-2001
              (NADP+ dependent), methenyltetrahydrofolate dehydrogenase
              formyltetrahydrofolate synthetase, clone MGC:15453 IMAGE:2960864,
              mRNA, complete cds.
BC017477
BC017477.1 GI:17028347
MGC.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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accession BC017477.1 GI:17028347
 version 1
 keywords mRNA, complete cds.
 source human.
 organism Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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| | | |
|----|------|--|
| OY | 1044 | aatggctccatgacaatgagcatccacgttggaaacacgcga |
| Db | 1118 | AAAGGCTCCACGCAATAGACCATSCAGTGGAAAACAGCCCA |
| OY | 1104 | gaggtacatttggccttaagctcaacggaagcagaagac |
| Db | 178 | GAGGCTCATTTGGGCTAGGCTCACCCTAAGCAGCAAGAC |
| OY | 1164 | caaccagaactactctctcgaacgagccatgctctctg |
| Db | 238 | CACACAGACATCACTTTCTCAACGCTCCATGACTTCCTG |
| OY | 1224 | ggctctccaagaatatacttggtgagcatattgagaagat |
| Db | 298 | GGCTCTCCAGAAATACATTTTGGTGGATCTATTGAGGAAT |
| OY | 1284 | gcagctctggaattcagaacatggtcagtagtgaagaga |
| Db | 358 | GCAGCTCTCCGAATTCACAAATAGGTCAGTAGTGGAAAGAGA |
| OY | 1344 | caacaggctgtagaacttcattgatttgaacttaagctctc |
| Db | 418 | CACAGCGGTGAGACTTCACTGCTTAAATTCACAGCTCTC |